

SEQUENCE LISTING

<110> Winslow, Barbara J.
Cochran, Mark D.

<120> Recombinant Virus Expressing Foreign DNA Encoding
Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
Feline Interferon-gama And Uses Thereof

<130> 54957-B

<140> Not Yet Known
<141> 1999-04-30

<150> 60/083,870
<151> 1998-05-01

<160> 82

<170> PatentIn Ver. 2.0

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<212> DNA
<213> feline CD80

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<222> (1)..(876)

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ccc aag ctc ttt ccg ctc ttg atg cta gct agt ctt ttt tac ttc tgt 96
Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
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tca ggt atc atc cag gtg aac aag aca gtg gaa gaa gta gca gta cta 144
Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu
35 40 45

tcc tgt gat tac aac att tcc acc aaa gaa ctg acg gaa att cga atc 192
Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile
50 55 60

tat tgg caa aag gat gat gaa atg gtg ttg gct gtc atg tct ggc aaa 240

Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys			
65	70	75	80
gta caa gtg tgg ccc aag tac aag aac cgc aca ttc act gac gtc acc			288
Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr			
85	90	95	
gat aac cac tcc att gtg atc atg gct ctg cgc ctg tca gac aat ggc			336
Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly			
100	105	110	
aaa tac act tgt att att caa aag att gaa aaa ggg tct tac aaa gtg			384
Lys Tyr Thr Cys Ile Ile Gln Lys Ile Glu Lys Gly Ser Tyr Lys Val			
115	120	125	
aaa cac ctg act tcg gtg atg tta ttg gtc aga gct gac ttc cct gtc			432
Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val			
130	135	140	
cct agt ata act gat ctt gga aat cca tct cat aac atc aaa agg ata			480
Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile			
145	150	155	160
atg tgc tta act tct gga ggt ttt cca aag cct cac ctc tcc tgg ctg			528
Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu			
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Glu Asn Glu Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp			
180	185	190	
cct gaa act gag ctc tac act att agc agt gaa ctg gat ttc aat atg			624
Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met			
195	200	205	
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Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn			
225	230	235	240
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Asn Gln Leu Trp Ile Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val			
245	250	255	
gtg atc act gca ctt acc tta aga tgc cta gtc cac aga cct gct gca			816

Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala			
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Arg Trp Arg Gln Arg Glu Met Gly Arg Ala Arg Lys Trp Lys Arg Ser			
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His Leu Ser Thr			
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Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys			
65	70	75	80
Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr			
85	90	95	
Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly			
100	105	110	
Lys Tyr Thr Cys Ile Ile Gln Lys Ile Glu Lys Gly Ser Tyr Lys Val			
115	120	125	
Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val			
130	135	140	
Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile			

145 150 155 160

Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190

Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met
195 200 205

Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr Gly Asn Leu Leu
210 215 220

Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn
225 230 235 240

Asn Gln Leu Trp Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val
245 250 255

Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala
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His Leu Ser Thr
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ccc aag ctc ttt ccg ctc ttg atg cta gct agt ctt ttt tac ttc tgt 96
Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
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tca ggt atc atc cag gtg aac aag aca gtg gaa gaa gta gca gta cta	35	40	45	144
Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu				
tcc tgt gat tac aac att tcc acc aaa gaa ctg acg gaa att cga atc	50	55	60	192
Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile				
tat tgg caa aag gat gat gaa atg gtg ttg gct gtc atg tct ggc aaa	65	70	75	240
Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys				
gta caa gtg tgg ccc aag tac aag aac cgc aca ttc act gac gtc acc	85	90	95	288
Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr				
gat aac cac tcc att gtg atc atg gct ctg cgc ctg tca gac aat ggc	100	105	110	336
Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly				
aaa tac act tgt atc att caa aag att caa aaa ggg tct tac aaa gtg	115	120	125	384
Lys Tyr Thr Cys Ile Ile Gln Lys Ile Gln Lys Gly Ser Tyr Lys Val				
aaa cac ctg act tcg gtg atg tta ttg gtc aga gct gac ttc cct gtc	130	135	140	432
Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val				
cct agt ata act gat ctt gga aat cca tct cat aac atc aaa agg ata	145	150	155	480
Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile				
atg tgc tta act tct gga ggt ttt cca aag cct cac ctc tcc tgg ctg	165	170	175	528
Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu				
gaa aat gaa gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat	180	185	190	576
Glu Asn Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp				
cct gaa act gag ctc tac act att agc agt gaa ctg gat ttc aat atg	195	200	205	624
Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met				
aca aac aac cat agc ttc ctg tgt ctt gtc aag tat gga aac tta ata	210	215	220	672
Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr Gly Asn Leu Ile				

gta tca cag atc ttc aac tgg caa aaa tca gag cca cag cct tct aat			720
Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn			
225	230	235	240
aat cag ctc tgg atc att atc ctg agc tca gta gta agt ggg att gtt			768
Asn Gln Leu Trp Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val			
245	250	255	
gtg atc act gca ctt acc tta aga tgc cta gtc cac aga cct gct gca			816
Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala			
260	265	270	
agg tgg aga caa aga gaa atg ggg aga gcg cgg aaa tgg aaa aga tct			864
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Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile			
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Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys			
65	70	75	80
Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr			
85	90	95	
Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly			
100	105	110	

Lys Tyr Thr Cys Ile Ile Gln Lys Ile Gln Lys Gly Ser Tyr Lys Val
115 120 125

Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val
130 135 140

Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile
145 150 155 160

Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190

Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met
195 200 205

Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr Gly Asn Leu Ile
210 215 220

Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn
225 230 235 240

Asn Gln Leu Trp Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val
245 250 255

Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala
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His Leu Ser Thr
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Met Gly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu	
1 5 10 15	
gtg atg gcc ctc ctg ctc tct ggt gtt tct tcc atg aag agt caa gca	155
Val Met Ala Leu Leu Leu Ser Gly Val Ser Ser Met Lys Ser Gln Ala	
20 25 30	
tat ttc aac aag act gga gaa ctg cca tgc cat ttt aca aac tct caa	203
Tyr Phe Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln	
35 40 45	
aac ata agc ctg gat gag ctg gta ttt tgg cag gac cag gat aag	251
Asn Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys	
50 55 60	
ctg gtt ctg tat gag ata ttc aga ggc aaa gag aac cct caa aat gtt	299
Leu Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val	
65 70 75	
cat ctc aaa tat aag ggc cgt aca agc ttt gac aag gac aac tgg acc	347
His Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr	
80 85 90 95	
ctg aga ctc cac aat gtt cag atc aag gac aag ggc aca tat cac tgt	395
Leu Arg Leu His Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys	
100 105 110	
ttc att cat tat aaa ggg ccc aaa gga cta gtt ccc atg cac caa atg	443
Phe Ile His Tyr Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met	
115 120 125	
agt tct gac cta tca gtg ctt gct aac ttc agt caa cct gaa ata aca	491
Ser Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Thr	
130 135 140	
gta act tct aat aga aca gaa aat tct ggc atc ata aat ttg acc tgc	539
Val Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys	
145 150 155	
tca tct ata caa ggt tac cca gaa cct aag gag atg tat ttt cag cta	587
Ser Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu	
160 165 170 175	
aac act gag aat tca act act aag tat gat act gtc atg aag aaa tct	635
Asn Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser	
180 185 190	

caa aat aat gtg aca gaa ctg tac aac gtt tct atc agc ttg cct ttt			683
Gln Asn Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe			
195	200	205	
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Ser Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu			
210	215	220	
gag aca ctg gag atg ctg ctc tcc cta cct ttc aat ata gat gca caa			779
Glu Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln			
225	230	235	
cct aag gat aaa gac cct gaa caa ggc cac ttc ctc tgg att gcg gct			827
Pro Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala			
240	245	250	255
gta ctt gta atg ttt gtt gtt ttt tgt ggg atg gtg tcc ttt aaa aca			875
Val Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr			
260	265	270	
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275	280	285	
acc atc aaa agg gag aga aaa gag agc aaa cag acc aac gaa aga gta			971
Thr Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val			
290	295	300	
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Pro Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile			
305	310	315	
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50	55	60
Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val His		
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Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu		
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Arg Leu His Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys Phe		
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Ile His Tyr Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Ser		
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Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Thr Val		
130	135	140
Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser		
145	150	155
Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn		
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Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Ser Gln		
180	185	190
Asn Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser		
195	200	205
Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu		
210	215	220
Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro		
225	230	235
Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val		
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Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu		
260	265	270

Arg Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr
275 280 285

Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro
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<212> DNA

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<220>

<221> CDS

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gta aca gaa aac aag att ttg gtg aag cag ttg ccc agg ctt gtg gtg 96
Val Thr Glu Asn Lys Ile Leu Val Lys Gln Leu Pro Arg Leu Val Val
20 25 30

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Tyr Asn Asn Glu Val Asn Leu Ser Cys Lys Tyr Thr His Asn Phe Phé
35 40 45

tca aag gag ttc cgg gca tcc ctt tat aag gga gta gat agt gct gtg 192
Ser Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asp Ser Ala Val
50 55 60

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Glu Val Cys Val Val Asn Gly Asn Tyr Ser His Gln Pro Gln Phe Tyr
65 70 75 80

tca agt aca gga ttc gac tgt gat ggg aaa ttg ggc aat gaa aca gtg 288
Ser Ser Thr Gly Phe Asp Cys Asp Gly Lys Leu Gly Asn Glu Thr Val
85 90 95

aca ttc tac ctc cga aat ttg ttt gtt aac caa acg gat att tac ttc	336		
Thr Phe Tyr Leu Arg Asn Leu Phe Val Asn Gln Thr Asp Ile Tyr Phe			
100	105	110	
tgc aaa att gaa gtc atg tat cca cct cct tac ata gac aat gag aag	384		
Cys Lys Ile Glu Val Met Tyr Pro Pro Tyr Ile Asp Asn Glu Lys			
115	120	125	
agc aat ggg acc att atc cac gtg aaa gag aaa cat ctt tgt cca gct	432		
Ser Asn Gly Thr Ile Ile His Val Lys Glu Lys His Leu Cys Pro Ala			
130	135	140	
cag ctg tct cct gaa tct tcc aag cca ttt tgg gca ctg gtg gtt	480		
Gln Leu Ser Pro Glu Ser Ser Lys Pro Phe Trp Ala Leu Val Val Val			
145	150	155	160
ggt gga atc cta ggt ttc tac agc ttg cta gca aca gtg gct ctt ggt	528		
Gly Gly Ile Leu Gly Phe Tyr Ser Leu Leu Ala Thr Val Ala Leu Gly			
165	170	175	
gct tgc tgg atg aag acc aag agg agt agg atc ctt cag agt gac tat	576		
Ala Cys Trp Met Lys Thr Lys Arg Ser Arg Ile Leu Gln Ser Asp Tyr			
180	185	190	
atg aac atg acc ccc cgg agg cca ggg ccc acc cga agg cac tac caa	624		
Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Arg His Tyr Gln			
195	200	205	
cct tac gcc cca gca cgc gac ttt gcg gca tac cgt tcc tgacatggac	673		
Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Ser			
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 20 25 30
 Tyr Asn Asn Glu Val Asn Leu Ser Cys Lys Tyr Thr His Asn Phe Phe

35

40

45

Ser Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asp Ser Ala Val
 50 55 60

Glu Val Cys Val Val Asn Gly Asn Tyr Ser His Gln Pro Gln Phe Tyr
 65 70 75 80

Ser Ser Thr Gly Phe Asp Cys Asp Gly Lys Leu Gly Asn Glu Thr Val
 85 90 95

Thr Phe Tyr Leu Arg Asn Leu Phe Val Asn Gln Thr Asp Ile Tyr Phe
 100 105 110

Cys Lys Ile Glu Val Met Tyr Pro Pro Tyr Ile Asp Asn Glu Lys
 115 120 125

Ser Asn Gly Thr Ile Ile His Val Lys Glu Lys His Leu Cys Pro Ala
 130 135 140

Gln Leu Ser Pro Glu Ser Ser Lys Pro Phe Trp Ala Leu Val Val Val
 145 150 155 160

Gly Gly Ile Leu Gly Phe Tyr Ser Leu Leu Ala Thr Val Ala Leu Gly
 165 170 175

Ala Cys Trp Met Lys Thr Lys Arg Ser Arg Ile Leu Gln Ser Asp Tyr
 180 185 190

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Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Ser
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<210> 9

<211> 749

<212> DNA

<213> feline CTLA-4

<220>

<221> CDS

<222> (27)..(698)

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Gly Ala Gln Leu Asp Leu Ala Ser Arg Thr Trp Pro Cys Thr Ala Leu	
10 15 20 25	
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Phe Ser Leu Leu Phe Ile Pro Val Phe Ser Lys Gly Met His Val Ala	
30 35 40	
cac cct gca gtg gtg ctg gcc agc agc cga ggt gtc gcc agc ttc gtg	197
His Pro Ala Val Val Leu Ala Ser Ser Arg Gly Val Ala Ser Phe Val	
45 50 55	
tgt gaa tat ggg tct tca ggc aat gcc gcc aaa ttc cga gtg act gtg	245
Cys Glu Tyr Gly Ser Ser Gly Asn Ala Ala Lys Phe Arg Val Thr Val	
60 65 70	
ctg agg caa act ggc agc caa atg act gaa gtc tgt gct gcg aca tac	293
Leu Arg Gln Thr Gly Ser Gln Met Thr Glu Val Cys Ala Ala Thr Tyr	
75 80 85	
aca gtg gag aat gag ttg gcc ttc cta aat gat tcc acc tgc act ggc	341
Thr Val Glu Asn Glu Leu Ala Phe Leu Asn Asp Ser Thr Cys Thr Gly	
90 95 100 105	
atc tcc agc gga aac aaa gtg aac ctc acc atc caa ggg ttg agg gcc	389
Ile Ser Ser Gly Asn Lys Val Asn Leu Thr Ile Gln Gly Leu Arg Ala	
110 115 120	
atg gac acg gga ctc tac atc tgc aag gtg gag ctc atg tac cca cca	437
Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro	
125 130 135	
ccc tac tat gca ggc atg ggc aat gga acc cag att tat gtc atc gat	485
Pro Tyr Tyr Ala Gly Met Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp	
140 145 150	
cct gaa cct tgc cca gat tct gac ttc ctc ctc tgg atc ctc gca gca	533
Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu Trp Ile Leu Ala Ala	
155 160 165	
gtc agt tca gga ttg ttt tat agc ttc ctt atc aca gct gtt tct	581
Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe Leu Ile Thr Ala Val Ser	
170 175 180 185	
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Leu Ser Lys Met Leu Lys Lys Arg Ser Pro Leu Thr Thr Gly Val Tyr	

190

195

200

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 Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu Lys Gln Phe Gln Pro
 205 210 215

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ccaatttctta agagctgagg c 749

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 35 40 45

Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly
 50 55 60

Asn Ala Ala Lys Phe Arg Val Thr Val Leu Arg Gln Thr Gly Ser Gln
 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu Leu Ala
 85 90 95

Phe Leu Asn Asp Ser Thr Cys Thr Gly Ile Ser Ser Gly Asn Lys Val
 100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Ala Gly Met Gly
 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
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